REMARKS/ARGUMENTS

Claims 3, and 11-18 are active in this application. Claims 3, 11, 12, and 14-16 are drawn to the elected subject matter. Support for the amendment to claim 3 is found in Claim 4 and the specification on page 10, line 20 to page 12, line 2; and page 16, line 10 to page 21. No new matter is believed to have been added by these amendments.

The pending claims are directed to an isolated and purified DNA comprising a sequence which hybridizes under specified to SEQ ID NO:1 and encodes a transcription factor which binds to a common sequence CCA(A/C)C(A/T)A(A/C)C(C/T)CC and which controls a phenylpropanoid biosynthesis pathway.

The rejection of Claims 3-4, 11-12, and 14-16 under 35 U.S.C. § 112, first paragraph ("written description") is respectfully traversed.

The application and claims define the DNA based on its structural relationship to SEQ ID NO:1, i.e., stringent hybridization conditions, and the activity of the protein encoded by the DNA, a transcription factor which controls a phenylpropanoid biosynthesis pathway and which binds to a common sequence as set forth in the claims and specification. SEQ ID NO:1 is unquestionably described (see the sequence listing). The activity of the protein encoded thereby is also described in the specification on page 10, line 20 to page 12, line 2; and page 16, line 10 to page 21. In particular, Applicants note the binding activity is described in page 22, line 1 to page 23, line 7.

Furthermore, the protein encoded by SEQ ID NO:1, i.e., SEQ ID NO:2 is also described in the specification (Sequence Listing). If one reverse translates the amino acid sequence into a DNA sequence, using the variations of the triplet codon numerous DNA sequences that encode SEQ ID NO:2 can be envisioned by one of ordinary skill in the art.

Therefore, this description that is inherent from the DNAs which encode SEQ ID NO:2 add the representative DNAs described in the present application.

Applicants also direct the Office's attention to Example 9 of the Synopsis of Application of Written Description Guidelines which analyzes a situation where a claim covers a genus of nucleotide sequences that hybridize under stringent conditions to a disclosed sequence having a particular activity. In these guidelines, the Patent Office has concluded that such a claim is adequately described within the meaning of 35 U.S.C. § 112, first paragraph. In particular, note the Patent Office's rationale:

> The claim is drawn to a genus of nucleic acids all of which must hybridize with SEQ ID NO:1 and must encode a protein with a specific activity.
>
> The search of the prior art indicates that SEQ ID NO:1 is novel and unobvious.
>
> There is a single species disclosed (a molecular consisting of SEQ ID NO:1) that is within the scope of the claimed genus.
>
> There is actual reduction to practice of the disclosed species.
>
> Now turning to the genus analysis, a person of skill in the art would not expect substantial variation among species encompassed within the scope of the claims because the highly stringent hydridization conditions set forth in the claim yield structurally similar DNAs. Thus, a representative number of species is disclosed, since highly stringent hydridization conditions in combination with the coding function of DNA and the level of skill and knowledge in the art are adequate to determine that applicant was in possession of the claimed invention.
>
> **Conclusion**: The claimed invention is adequately described.

In view of this guidance provided by the Patent Office and the above-noted description explicitly provided in the specification, the present claims are described.

Withdrawal of this ground of rejection is requested.

The rejection of Claims 3-4, 11-12, and 14-16 under 35 U.S.C. § 112, first paragraph ("enablement") is respectfully traversed.

As noted above, the specification describes the polynucleotides claimed. Furthermore, the discussion of stringent conditions is found on page 7, second paragraph, of this application, the application describes the protein encoded by the DNA as a transcription factor which controls a phenylpropanoid biosynthesis pathway and which binds to a common sequence as set forth in the claims and specification. The activity of the protein encoded thereby is also described in the specification on page 10, line 20 to page 12, line 2; and page 16, line 10 to page 21. In particular, Applicants note the binding activity is described in page 22, line 1 to page 23, line 7. In view of this, one would simply have to isolate a DNA and test for the ability of the protein encoded thereby to bind to the noted sequence and control a phenylproanoid biosynthesis pathyway.

Withdrawal of this ground of rejection is requested.

The rejection of Claims 3-4, 11-12, and 14-16 under 35 U.S.C. § 102(b) over Tamagnone et al is respectfully traversed.

Tamagnone does not describe any specific nucleotide sequence but recombinant molecules contained in a vector. Thus, there does not appear to be any basis to allege that recombinant vectors in Tamagnone have any similarity to or would hybridize to SEQ ID NO:1 under the specified conditions and the activity of the protein encoded by the DNA as a transcription factor which controls a phenylpropanoid biosynthesis pathway and which binds to a common sequence as set forth in the claims. Further, a search of the publically available PubMed protein databases for the two Myb genes in Tamagnone, i.e., AmMYB308 and AmMYB330 did not identify any specific DNA or protein sequence for these genes. The only sequence identified relates to a promoter region of these genes (ACCESSION:Y15607,

Antirrhinum majus 4CL gene, promoter region). Applicants also performed a search of the database of *Arabodopsis thaliana*-derived DNA encoding MYB transcription factors and identified a sequence (Atmyb2: Accession number D14712). The homology of this myb transcription factor and SEQ ID NO:2 is relatively low as evidenced by the alignment of these two proteins below:

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                  *         20         *         40         *         60
SEQ 2  :  MAFAGTTQKCMACDKTVYLVDKLTADNRIYHKACFRCHHCKGTVKLGNYNSEEGVLYCREHFDQ  :  64
D14712 :  MEDYERINSNSPTHEEDSDVRKGPWTEEEDAILVNFVSIHGDARWNHIARSSGLKRTGKSCRLR  :  64
          M                    V K                                S    4

                  *         80         *         100        *         120
SEQ 2  :  LFKQTGSLDKSFEGTPKIVKPQKPIDSEKPQVAKVTSMPGGTREKCFGCKKTVYPTEKVSANGT  :  128
D14712 :  WLNYLRPDVRRGNITLEEQFMILKLHSLWGNRWSKIAQYLPGRTDNEIKNYWRTRVQKQAKHLR  :  128
                    4    T          6 S          5   R              2K

                  *         140        *         160        *         180        *
SEQ 2  :  PYHKSCFQCSHGGCVISPSNYTAHEGRLYCKHHHIQLIKEKGNLSKLEGDHEWNSTTTTEVTAE  :  192
D14712 :  CDVNSNLEKETMRNVWMPRLVERINAQSLPTTCEQVESMITDPSQPVNEPSPVEPGFVQFSQNH  :  192
              S          V  P                                    6     6

                  200        *         220        *         240        *
SEQ 2  :  SYTADQVD----------------------------------------------------------  :  200
D14712 :  HQQFVPATELSATSSNSPAETFSDVRGGVVNGSGYDPSGQTGFGEFNDWGCVGGDNMWTDEESF  :  256

                  260        *
SEQ 2  :  ------------------  :  -
D14712 :  WFLQDQFCPDTTSYSYN  :  273
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Therefore, as the myb transcription factor from a plant has little homology to SEQ ID NO:2, it logically flows that the DNAs encoding the myb factor and SEQ ID NO:1 would also have relatively low homology. Therefore, Applicants submit that Tamagnone does not describe a DNA which would hybridize to SEQ ID NO:1 under the specified conditions and encode a transcription factor protein which controls a phenylpropanoid biosynthesis pathway and which binds to a common sequence as set forth in the claims.

Accordingly, withdrawal of this rejection is requested.

Concerning the rejection under the doctrine of obviousness type double patenting over the parental application, now U.S. patent no. 6,303,847, Applicants respectfully traverse the rejection but may consider filing a Terminal Disclaimer once the Patent Office finds the pending claims otherwise allowable.

Applicants request an indication that the pending claims are allowable.

Respectfully submitted,

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